GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: May 18, 2002, 02:17:21 ; Search time 733.22 Seconds
(without alignments)
2528.938 Million cell updates/sec

Title: US-09-719-748-1_COPY_62_1141
Perfect score: 1080
Sequence: 1 atggagccattcaagcagca.....ggaggaggagcagcacctcc 1080

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*
1: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
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3: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT:*
4: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
5: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1984.DAT:*
6: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
7: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1986.DAT:*
8: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1987.DAT:*
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23: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*
24: /net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1080	100.0	1742	21	AAZ49765	Human DAP-kinase-r
2	1012	93.7	1253	23	AAS73461	DNA encoding novel
3	516.2	47.8	2079	22	AAK94258	Human full-length
4	514.6	47.6	2132	20	AAX34656	Human ZIP-kinase (
5	514.6	47.6	2224	22	AAH16158	Human cDNA sequenc
6	514.6	47.6	2224	22	AAH78068	Nucleotide sequenc
7	512.8	47.5	1429	20	AAX34657	Murine ZIP-kinase
8	448.6	41.5	4272	16	AAQ89839	Human death associ
9	448.6	41.5	5886	16	AAQ89838	Human death associ
10	448.6	41.5	5886	19	AAV60289	DNA sequence encod
11	445.4	41.2	480	21	AAZ99731	cDNA encoding huma
12	445.4	41.2	1864	21	AAZ99730	cDNA encoding huma
13	385	35.6	757	22	AAK91856	Human cDNA 5'-end
14	385	35.6	757	22	AAK93262	Human cDNA clone r
15	244.6	22.6	12638	22	AAK70641	Human immune/haema
16	238.4	22.1	1120	22	ABA09608	Human bone marrow
17	238.4	22.1	1505	22	ABA09692	Human bone marrow
18	202.8	18.8	3192	21	AAF16067	Human prostate can
19	189.8	17.6	539	22	AAH06178	Human cDNA clone (
20	187.2	17.3	873	22	AAH46902	cDNA encoding huma
21	177	16.4	1776	22	AAF44679	Novel protein kina
22	167.8	15.5	2562	23	ABL03417	Drosophila melanog
23	166.8	15.4	3284	23	ABL18303	Drosophila melanog
24	166.8	15.4	3374	23	ABL11987	Drosophila melanog
25	165.8	15.4	1836	22	AAS06721	Polynucleotide seq
26	165.8	15.4	2046	22	AAH78263	Nucleotide sequenc
27	165.8	15.4	2671	22	AAF44650	Novel protein kina
28	164.2	15.2	1839	24	AAD26573	Human POLY4 cDNA.
29	164.2	15.2	2625	22	AAF44661	Novel protein kina
30	164.2	15.2	5532	20	AAZ25100	Human ischaemic he
31	163.4	15.1	3864	22	AAF44664	Novel protein kina
32	163.4	15.1	5355	20	AAX89220	Seq ID No: 28 of W
c 33	163.4	15.1	5355	20	AAX89221	Seq ID No: 30 of W
34	163.4	15.1	5355	21	AAZ39404	Human Trad protein
c 35	163.4	15.1	5355	21	AAZ39405	Human Trad protein
36	162.8	15.1	1971	24	AAD26571	Human POLY2 cDNA.
37	162.8	15.1	2558	24	AAD26572	Human POLY3 cDNA.
38	161.4	14.9	1917	23	ABL03333	Drosophila melanog
39	154.6	14.3	2973	24	AAD26453	Human kinase PKIN-
40	154	14.3	513	22	ABA60848	Human foetal liver
41	154	14.3	513	22	ABA28854	Probe #7320 for ge
42	154	14.3	513	22	AAK09135	Human brain expres
43	154	14.3	513	22	AAK35024	Human bone marrow
44	154	14.3	513	22	AAI16902	Probe #6835 for ge
45	154	14.3	513	22	AAI40741	Probe #9427 used t

ALIGNMENTS

RESULT 1
AAZ49765
ID AAZ49765 standard; DNA; 1742 BP.
XX
AC AAZ49765;
XX
DT 18-APR-2000 (first entry)
XX
DE Human DAP-kinase-related protein 1 (DRP-1) encoding DNA.
XX
KW DAP-kinase-related protein 1; DRP-1; Death-Associated Protein;
KW calmodulin-dependent serine/threonine kinase; apoptosis; dimerisation;
KW cytostatic; antipsoriatic; immunosuppressive; metastasis; tumour; human;
KW treatment; cancer; psoriasis; autoimmune disease; screening; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 62..1144
FT /*tag= a
FT /product= "DAP-kinase-related protein 1"
FT polyA_signal 1720..1725
FT /*tag= b
XX
PN WO9966030-A1.
XX
PD 23-DEC-1999.
XX
PF 15-JUN-1999; 99WO-US13411.
XX
PR 15-JUN-1998; 98US-0089294.
XX

```
PA   (YEDA ) YEDA RES & DEV CO LTD.
PA   (MCIN/) MCINNIS P A.
XX
PI   Kimchi A;
XX
DR   WPI; 2000-147148/13.
DR   P-PSDB; AAY44674.
XX
PT   Calmodulin-dependent serine/threonine kinase capable of inducing
PT   apoptosis used in the treatment of e.g. cancer -
XX
PS   Claim 3; Fig 1; 67pp; English.
XX
CC   The present sequence encodes DAP (death-associated protein)-
CC   kinase-related protein 1 (DRP-1), which is a calmodulin-dependent
CC   serine/threonine kinase. DRP-1 is a cytoplasmic protein capable of
CC   inducing apoptosis by dimerisation. It shows significant homology to
CC   DAP kinase. It has cytostatic, antipsoriatic and immunosuppressive
CC   activity and can be used for inhibiting growth/metastasis of
CC   tumours and promoting death of tumour cells. It can also be used in
CC   the treatment of cancer, psoriasis and autoimmune diseases. Fragments
CC   of DRP-1 DNA are useful as probes for screening individuals with a
CC   predisposition to cancer.
XX
SQ   Sequence 1742 BP; 442 A; 437 C; 504 G; 359 T; 0 other;

  Query Match             100.0%;  Score 1080;  DB 21;  Length 1742;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-289;
  Matches 1080;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
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Db     62 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 121

Qy     61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
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Qy    181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 301

Qy    241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
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Db    302 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 361

Qy    301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
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Qy    361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
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Db    422 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 481

Qy    421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
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Db    482 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 541

Qy    481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
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Qy    541 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    601 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccttcctgggagac 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    661 acgaagcaggaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
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Qy    721 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    782 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 841

Qy    781 cggaaacggctcacaatccaagaggctctcagacacccctggatcacgccggtggacaac 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    901 gtccgcaggcggtggaagctttccttcagcatcgtgtccctgtgcaaccacctcacccgc 960
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Qy    961 tcgctgatgaagaaggtgcacctgaggccggatgaggacctgaggaactgtgagagtgac 1020
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Qy   1021 actgaggaggacatcgccaggaggaaagccctccacccacggaggaggagcagcacctcc 1080
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Db   1082 actgaggaggacatcgccaggaggaaagccctccacccacggaggaggagcagcacctcc 1141

RESULT   2
AAS73461
ID   AAS73461 standard; cDNA; 1253 BP.
XX
AC   AAS73461;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #9265.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG09274.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 9265; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
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CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1253 BP; 331 A; 303 C; 366 G; 253 T; 0 other;

  Query Match            93.7%;  Score 1012;  DB 23;  Length 1253;
  Best Local Similarity  99.5%;  Pred. No. 2e-270;
  Matches 1015;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Qy     121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
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Qy     181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
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Qy     241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
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Qy     301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
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Qy     361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
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Qy     421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
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Db     591 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 650

Qy     481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
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Qy     541 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     711 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 770

Qy     601 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagac 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     771 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagac 830

Qy     661 acgaagcaggaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     831 acgaagcaggaaacactggcaaatatcacagcagtgagttacgactttgatgaggaattc 890

Qy     721 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 780
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     891 ttcagccagacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 950

Qy     781 cggaaacggctcacaatccaagaggctctcagacacccctggatcacgccggtggacaac 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     951 cggaaacggctcacaatccaagaggctctcagacacccctggatcacgccggtggacaac 1010

Qy     841 cagcaagccatggtgcgacgggagtctgtggtcaatctggagaacttcaggaagcagtat 900
           |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db    1011 cagcaagccatggtgcgcagggagtctgtggtcaatctggagaacttcaggaagcagtat 1070

Qy     901 gtccgcaggcggtggaagctttccttcagcatcgtgtccctgtgcaaccacctcacccgc 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     961 tcgctgatgaagaaggtgcacctgaggccggatgaggacctgaggaactgtgagagtgac 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1021 actgaggaggacatcgccaggaggaaagccctccacccacggaggaggagcagcacctcc 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1191 actgaggaggacatcgccaggaggaaagccctccacccacggaggaggagcagcacctcc 1250

RESULT   3
AAK94258
ID   AAK94258 standard; cDNA; 2079 BP.
XX
AC   AAK94258;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human full-length cDNA, SEQ ID NO: 2874.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   P-PSDB; AAM93338.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Claim 8; SEQ ID NO 2874; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC   molecules have been determined. Primers for synthesising the full length
CC   cDNA are useful for clarifying the function of the protein encoded by
CC   the cDNA. The full length clones were obtained by construction of full
CC   length enriched cDNA libraries that were synthesised by the oligo-capping
CC   method. The primers enable the production of the full length cDNA easily
CC   without any special methods. The present sequence is a full length
CC   human cDNA of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ   Sequence 2079 BP; 396 A; 626 C; 733 G; 324 T; 0 other;
```

Query Match 47.8%; Score 516.2; DB 22; Length 2079;
Best Local Similarity 76.2%; Pred. No. 8.4e-133;
Matches 635; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Qy       1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
Db      70 atgtccacgttcaggcaggaggacgtggaggaccattatgagatgggggaggagctgggc 129
Qy      61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
Db     130 agcggccagtttgcgatcgtgcggaagtgccggcagaagggcacgggcaaggagtacgca 189
Qy     121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
Db     190 gccaagttcatcaagaagcgccgcctgtcatccagccggcgtggggtgagccgggaggag 249
Qy     181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
Db     250 atcgagcgggaggtgaacatcctgcgggagatccggcaccccaacatcatcaccctgcac 309
Qy     241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
Db     310 gacatcttcgagaacaagacggacgtggtcctcatcctggagctggtctctggcggggag 369
Qy     301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
Db     370 ctctttgacttcctggcggagaaggagtcgctgacggaggacgaggccacccagttcctc 429
Qy     361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
Db     430 aagcagatcctggacggcgttcactacctgcactctaagcgcatcgcacactttgacctg 489
Qy     421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
Db     490 aagccggaaaacatcatgctgctggacaagaacgtgcccaacccacgaatcaagctcatc 549
Qy     481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
Db     550 gacttcggcatcgcgcacaagatcgaggcggggaacgagttcaagaacatcttcggcacc 609
Qy     541 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 600
Db     610 ccggagtttgtggccccagagattgtgaactatgagccgctgggcctggaggcggacatg 669
Qy     601 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccttttcctgggagac 660
Db     670 tggagcatcggtgtcatcacctatatcctcctgagcggtgcatccccgttcctgggcgag 729
Qy     661 acgaagcaggaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
Db     730 accaagcaggagacgctcaccaacatctcagccgtgaactacgacttcgacgaggagtac 789
Qy     721 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 780
Db     790 ttcagcaacaccagcgagctggccaaggacttcattcgccggctgctcgtcaaagatccc 849
Qy     781 cggaaacggctcacaatccaagaggctctcagacacccctggatcacgccggt 833
Db     850 aagcggagaatgaccattgcccagagcctggaacattcctggattaaggcgat 902
```

RESULT 4
AAX34656
ID AAX34656 standard; DNA; 2132 BP.
XX
AC AAX34656;
XX
DT 01-JUL-1999 (first entry)
XX
DE Human ZIP-kinase (serine/threonine kinase) encoding DNA.
XX
KW Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
KW Human; murine; ss.
XX
OS Homo sapiens.
XX
PN EP911408-A2.
XX
PD 28-APR-1999.
XX
PF 24-SEP-1998; 98EP-0307747.
XX
PR 26-SEP-1997; 97JP-0261589.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Akira S, Kawai T;
XX
DR WPI; 1999-246420/21.
DR P-PSDB; AAY06921.
XX
PT New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase)
PT protein and DNA, useful as anticancer agents
XX
PS Claim 5; Page 15-18; 33pp; English.
XX
CC The invention provides human and murine recombinant Zipper Interacting
CC Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine
CC kinases which bind the leucine zipper domain of transcription factor
CC ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic
CC acids are used for the recombinant expression of the proteins. ZIP-kinase
CC protein and DNA are useful as gene therapeutic agents against cancer, and
CC as anti-cancer agents. The present sequence represents a DNA encoding a
CC human ZIP kinase protein.
XX
SQ Sequence 2132 BP; 429 A; 630 C; 741 G; 332 T; 0 other;

Query Match 47.6%; Score 514.6; DB 20; Length 2132;
Best Local Similarity 76.1%; Pred. No. 2.4e-132;
Matches 634; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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Qy       1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
Db      94 atgtccacgttcaggcaggaggacgtggaggaccattatgagatgggggaggagctgggc 153
Qy      61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
Db     154 agcggccagtttgcgatcgtgcggaagtgccggcagaagggcacgggcaaggagtacgca 213
Qy     121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
Db     214 gccaagttcatcaagaagcgccgcctgtcatccagccggcgtggggtgagccgggaggag 273
Qy     181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
Db     274 atcgagcgggaggtgaacatcctgcgggagatccggcaccccaacatcatcaccctgcac 333
Qy     241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
Db     334 gacatcttcgagaacaagacggacgtggtcctcatcctggagctggtctctggcggggag 393
Qy     301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
Db     394 ctctttgacttcctggcggagaaagagtcgctgacggaggacgaggccacccagttcctc 453
Qy     361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
Db     454 aagcagatcctggacggcgttcactacctgcactctaagcgcatcgcacactttgacctg 513
Qy     421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
Db     514 aagccggaaaacatcatgctgctggacaagaacgtgcccaacccacgaatcaagctcatc 573
```

```
Qy    481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
Db    574 gacttcggcatcgcgcacaagatcgaggcggggaacgagttcaagaacatcttcggcacc 633

Qy    541 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 600
Db    634 ccggagtttgtggccccagagattgtgaactatgagccgctgggcctggaggcggacatg 693

Qy    601 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagac 660
Db    694 tggagcatcggtgtcatcacctatatcctcctgagcggtgcatccccgttcctgggcgag 753

Qy    661 acgaagcaggaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
Db    754 accaagcaggagacgctcaccaacatctcagccgtgaactacgacttcgacgaggagtac 813

Qy    721 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 780
Db    814 ttcagcaacaccagcgagctggccaaggacttcattcgccggctgctcgtcaaagatccc 873

Qy    781 cggaaacggctcacaatccaagaggctctcagacacccctggatcacgccggt 833
Db    874 aagcggagaatgaccattgcccagagcctggaacattcctggattaaggcgat 926
```

RESULT 5
AAH16158
ID AAH16158 standard; cDNA; 2224 BP.
XX
AC AAH16158;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14925.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 14925; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2224 BP; 419 A; 656 C; 806 G; 343 T; 0 other;

Query Match 47.6%; Score 514.6; DB 22; Length 2224;
Best Local Similarity 76.1%; Pred. No. 2.4e-132;
Matches 634; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

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Qy      1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
Db    215 atgtccacgttcaggcaggaggacgtggaggaccattatgagatgggggaggagctgggc 274

Qy     61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
Db    275 agcggccagtttgcgatcgtgcggaagtgccggcagaagggcacgggcaaggagtacgca 334

Qy    121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
Db    335 gccaagttcatcaagaagcgccgcctgtcatccagccggcgtggggtgagccgggaggag 394

Qy    181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
Db    395 atcgagcgggaggtgaacatcctgcgggagatccggcaccccaacatcatcaccctgcac 454

Qy    241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
Db    455 gacatcttcgagaacaagacggacgtggtcctcatcctggagctggtctctggcggggag 514

Qy    301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
Db    515 ctctttgacttcctggcggagaaggagtcgctgacggaggacgaggccacccagttcctc 574

Qy    361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
Db    575 aagcagatcctggacggcgttcactacctgcactctaagcgcatcgcacactttgacctg 634

Qy    421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
Db    635 aagccggaaaacatcatgctgctggacaagaacgtgcccaacccacgaatcaagctcatc 694

Qy    481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
Db    695 gacttcggcatcgcgcacaagatcgaggcggggaacgagttcaagaacatcttcggcacc 754

Qy    541 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 600
Db    755 ccggagtttgtggccccagagattgtgaactatgagccgctgggcctggaggcggacatg 814

Qy    601 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagac 660
Db    815 tggagcatcggtgtcatcacctatatcctcctgagcggtgcatccccgttcctgggcgag 874

Qy    661 acgaagcaggaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
Db    875 accaagcaggagacgctcaccaacatctcagccgtgaactacgacttcgacgaggagtac 934

Qy    721 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 780
Db    935 ttcagcaacaccggcgagctggccaaggacttcattcgccggctgctcgtcaaagatccc 994
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Qy    781 cggaaacggctcacaatccaagaggctctcagacacccctggatcacgccggt 833
          |    |  | || ||     ||   ||   |||  ||||||| | | || |
Db    995 aagcggagaatgaccattgcccagagcctggaacattcctggattaaggcgat 1047
```

RESULT 6
AAH78068
ID AAH78068 standard; DNA; 2224 BP.
XX
AC AAH78068;
XX
DT 26-NOV-2001 (first entry)
XX
DE Nucleotide sequence of a human protein kinase/protein phosphatase.
XX
KW Human; protein kinase; protein phosphatase; signal transduction;
KW intracellular signalling pathway; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 215..1579
FT /*tag= a
FT /product= "protein kinase/protein phosphatase"
XX
PN WO200109345-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-JP05060.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 18-OCT-1999; 99US-0159590.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
PR 02-MAY-2000; 2000JP-0183767.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX
DR WPI; 2001-564736/63.
DR P-PSDB; AAG67425.
XX
PT New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes -
XX
PS Claim 1; Page 119-125; 336pp; Japanese.
XX
CC The present sequence encodes a human protein kinase/protein
CC phosphatase. The polypeptides are expected to participate in signal
CC transduction in cells. The kinase phosphatases are connected with
CC intracellular signalling pathways. Antisense oligonucleotides and
CC compounds identified by screening (agonists or antagonists) can be
CC used to treat human or animal disorders associated with the expression
CC or function of the protein. In addition, the polypeptides may be used
CC as target molecules fir drug development.
XX
SQ Sequence 2224 BP; 419 A; 656 C; 806 G; 343 T; 0 other;

Query Match 47.6%; Score 514.6; DB 22; Length 2224;
Best Local Similarity 76.1%; Pred. No. 2.4e-132;
Matches 634; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

```
Qy      1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
          |||    | |||| |||| || | |||||||||  |||||| || || ||||||||||||
Db    215 atgtccacgttcaggcaggaggacgtggaggaccattatgagatgggggaggagctgggc 274

Qy     61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
          || |||||||||| |||||| |||||||||| ||||| |||||||    ||||| |||
Db    275 agcggccagtttgcgatcgtgcggaagtgccggcagaagggcacgggcaaggagtacgca 334

Qy    121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
          |||||||||||||||||||| |          | ||||||| || ||||||||||||||||
Db    335 gccaagttcatcaagaagcgccgcctgtcatccagccggcgtggggtgagccgggaggag 394

Qy    181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
          |||||||||||||||| |||||||||| || | | ||||| |||  |||||||  ||||||
Db    395 atcgagcgggaggtgaacatcctgcgggagatccggcaccccaacatcatcaccctgcac 454

Qy    241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
          ||| |||  ||||||   || |||||||| | ||||||  ||||| || ||||| || |||
Db    455 gacatcttcgagaacaagacggacgtggtcctcatcctggagctggtctctggcggggag 514

Qy    301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
          |||||  || ||||||||  |||||||||| ||||  |||||  |||||||||   ||| |
Db    515 ctctttgacttcctggcggagaaggagtcgctgacggaggacgaggccacccagttcctc 574

Qy    361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
          |||||||||||||| || ||  ||||||| ||| | |||   || || |||||||| ||
Db    575 aagcagatcctggacggcgttcactacctgcactctaagcgcatcgcacactttgacctg 634

Qy    421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
          |||||  |||||||| ||| || | ||||||||  | ||||  ||||  |||||||| ||
Db    635 aagccggaaaacatcatgctgctggacaagaacgtgcccaacccacgaatcaagctcatc 694

Qy    481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
          |||||  ||  | || ||| | || || |  ||    || || ||||| || || || ||
Db    695 gacttcggcatcgcgcacaagatcgaggcggggaacgagttcaagaacatcttcggcacc 754

Qy    541 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 600
          ||||| ||||| || ||||| |||||||||||| ||||| ||||| |||||||| ||||||
Db    755 ccggagtttgtggccccagagattgtgaactatgagccgctgggcctggaggcggacatg 814

Qy    601 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagac 660
          |||||||| || |||||||||| |||||| | || || |||||||| |||||||| ||
Db    815 tggagcatcggtgtcatcacctatatcctcctgagcggtgcatccccgttcctgggcgag 874

Qy    661 acgaagcaggaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
          || |||||||| || ||  | || ||| || | ||||  |||||||| || ||||| | |
Db    875 accaagcaggagacgctcaccaacatctcagccgtgaactacgacttcgacgaggagtac 934

Qy    721 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 780
          |||||| | ||  |||||||||||||||||| |||||   ||| || || |||||  ||
Db    935 ttcagcaacaccggcgagctggccaaggacttcattcgccggctgctcgtcaaagatccc 994

Qy    781 cggaaacggctcacaatccaagaggctctcagacacccctggatcacgccggt 833
          |    |  | || ||     ||   ||   |||  ||||||| | | || |
Db    995 aagcggagaatgaccattgcccagagcctggaacattcctggattaaggcgat 1047
```

RESULT 7
AAX34657
ID AAX34657 standard; DNA; 1429 BP.
XX
AC AAX34657;
XX
DT 01-JUL-1999 (first entry)
XX
DE Murine ZIP-kinase (serine/threonine kinase) encoding DNA.
XX
KW Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
KW Human; murine; ss.
XX
OS Mus musculus.
XX
PN EP911408-A2.
XX
PD 28-APR-1999.
XX

PF 24-SEP-1998; 98EP-0307747.
XX
PR 26-SEP-1997; 97JP-0261589.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Akira S, Kawai T;
XX
DR WPI; 1999-246420/21.
DR P-PSDB; AAY06922.
XX
PT New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase)
PT protein and DNA, useful as anticancer agents
XX
PS Claim 6; Page 19-22; 33pp; English.
XX
CC The invention provides human and murine recombinant Zipper Interacting
CC Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine
CC kinases which bind the leucine zipper domain of transcription factor
CC ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic
CC acids are used for the recombinant expression of the proteins. ZIP-kinase
CC protein and DNA are useful as gene therapeutic agents against cancer, and
CC as anti-cancer agents. The present sequence represents a DNA encoding a
CC murine ZIP kinase protein.
XX
SQ Sequence 1429 BP; 309 A; 425 C; 475 G; 220 T; 0 other;

Query Match 47.5%; Score 512.8; DB 20; Length 1429;
Best Local Similarity 76.2%; Pred. No. 6.1e-132;
Matches 631; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

```
Qy      1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
          |||    |||||| |||  || | || ||||||  |||||| || ||||||||||| ||
Db     10 atgtccacattcaggcaagaggatgttgaggaccattatgagatgggagaggagcttggc 69

Qy     61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
          |||||||| ||||||||||||   ||||||| | ||||| |||||||  | |||||||||
Db     70 agtggccaatttgccatcgtgcgcaagtgccagcagaagggcacgggcatggagtatgca 129

Qy    121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
          ||||||||||||||||||||||     |   | ||||||||||||||||||||||||||||
Db    130 gccaagttcatcaagaagcggcgcctgccatccagccggcgcggtgtgagccgggaggag 189

Qy    181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
          ||||| || ||||||||||||||||||  || | |  |||| |||  |||| || |||||
Db    190 atcgaacgcgaggtgagcatcctgcgcgagatccgccaccccaacatcataacactgcat 249

Qy    241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
          |||||  |  ||||||   || || |||||||  ||||| ||||| ||||| || || |||
Db    250 gacgtgttcgagaacaagacagatgtggtgctgatcctggagctggtgtccggtggcgag 309

Qy    301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
          || ||||| |||||||||| |||||||||||  |||  ||||| ||||||||    ||| |
Db    310 cttttcgacttcctggccgagaaggagtcattgacggaggatgaggccacgcagttcctc 369

Qy    361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
          || || ||||| || || ||  ||||||| ||| | |||   || || |||||||| ||
Db    370 aaacaaatcctagacggtgtccactacctgcactccaagcgcatcgcacactttgacctg 429

Qy    421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
          ||||| || ||||| ||||||  | ||||||  |     |||  || | ||| ||||| ||
Db    430 aagcccgagaacatcatgttgctggacaagcacgcagccagcccccgcattaagctcatc 489

Qy    481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
          ||||||||  | || |||   || || | |||    || || ||||| || ||||| ||
Db    490 gactttggcatcgcgcacaggatcgaggctggcagcgagttcaagaacatctttggcaca 549

Qy    541 ccggaatttgttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatg 600
          || || ||||| || || || || |||||||| ||||| || ||  ||||||||||||||
Db    550 cccgagtttgtcgcccccgagatcgtgaactatgagccacttggcttggaggctgacatg 609

Qy    601 tggagcataggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagac 660
          |||||||| |||||||||||||||||||| | || ||||| ||||| |||||||| ||
Db    610 tggagcattggcgtcatcacctacatcctcctgagcggagcgtccccattcctgggcgag 669

Qy    661 acgaagcaggaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
          || |||||||| || ||| | || ||| || ||||||  || ||||||||||||||| |
Db    670 accaagcaggagacgctgacgaacatctcagcagtgaactatgactttgatgaggaatac 729

Qy    721 ttcagccatacgagcgagctggccaaggactttattcggaagcttctggttaaagagacc 780
          ||||||   || |||||||||||||||||||| || || | ||| ||||| |||||  ||
Db    730 ttcagcagcaccagcgagctggccaaggacttcatccgcaggctgctggtcaaagacccc 789

Qy    781 cggaaacggctcacaatccaagaggctctcagacacccctggatcacg 828
            ||   || | || |||  | ||   ||    ||  ||||||||| |
Db    790 aagaggaggatgaccatcgcacagagcctggagcattcctggatcaag 837
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RESULT 8
AAQ89839
ID AAQ89839 standard; cDNA; 4272 BP.
XX
AC AAQ89839;
XX
DT 04-JAN-1980 (first entry)
XX
DE Human death associated protein DAP-2.
XX
KW Death associated protein; DAP; cytokine; cell death; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4272
FT /*tag= a
XX
PN WO9510630-A.
XX
PD 20-APR-1995.
XX
PF 12-OCT-1994; 94WO-US11598.
XX
PR 12-OCT-1993; 93IL-0107250.
XX
PA (RYCU/) RYCUS A.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Kimchi A;
XX
DR WPI; 1995-178528/23.
DR P-PSDB; AAR74205.
XX
PT DNA whose expression mediates cytokine-induced programmed cell
PT death - used to treat diseases or disorders associated with
PT uncontrolled, pathological cell growth or cytokine-induced
PT programmed cell death.
XX
PS Claim 2; Fig 8; 61pp; English.
XX
CC DAP genes seem to play an imp. role in programmed cell death and the
CC inhibition of their expression protects the cell from cytokine-
CC promoted cell death. A cDNA library was generated from a mixture of
CC mRNAs harvested after treatment of HeLa cells with IFN-gamma. It
CC was cloned in antisense orientation into the EBV-based pTK01
CC expression vector. The resulting expression library was introduced
CC into HeLa cells. A fraction of the transfectants was selected with
CC hygromycin B. The majority of transfected cells were selected with
CC both hygromycin B and IFN-gamma. The cells that survived and/or
CC grew in the presence of IFN-gamma were expanded and pooled. The
CC extrachromosomal DNA was obtd. and cleaved with DpnI and introduced
CC into E. coli HB101 host cells. A few bacterial clones were obtd.
CC which included DNA antisense sequences, some of which were able to
CC protect cells from the death-promoting effects of IFN-gamma.
CC Plasmid DNAs were prepd. from 10 individual bacterial clones. PCR
CC amplified cDNA inserts were generated from each plasmid using

```
CC   primers that corresp. to the immediate flanking sequence of the
CC   cDNA insertion sites in the pTK01 vector. The PCR fragments were
CC   used as labeled probes to seach Southern blots for possible cross
CC   hybridisation between some of the rescued antisense cDNA clones.
CC   The 10 cDNA clones were classified into six distinct
CC   non-overlapping gps., some constituting several members (clones)
CC   and some constituting a single member. Antisense cDNA clone 256 has
CC   the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and
CC   used to screen a K562 lambda gt10 cDNA library. The resulting
CC   composite sequence derived from 2 clones and the deduced AA sequence
CC   are shown in AAQ89838 and AAR74205. The ORF is also shown in AAQ89839.
CC   AAQ89838 has a poly A tail. The calculated mol. wt. of the protein
CC   is about 160 kDa. Several known domains and motifs were identified
CC   in the protein (see AAQ74205 FT).
XX
SQ   Sequence 4272 BP; 1076 A; 1161 C; 1121 G; 914 T; 0 other;

  Query Match           41.5%;  Score 448.6;  DB 16;  Length 4272;
  Best Local Similarity 67.5%;  Pred. No. 6.6e-114;
  Matches  659;  Conservative    0;  Mismatches  294;  Indels   24;  Gaps    1;

Qy      10 ttcaagcagcagaaggtggaggacttttatgacatcggagaggagctggggagtggccag 69
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Db      10 ttcaggcaggaaaacgtggatgattactacgacaccggcgaggaacttggcagtggacag 69

Qy      70 tttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgcagccaagttc 129
           |||||  | |||||||| ||||| ||||| || || || ||  ||||| | ||||| |||
Db      70 tttgcggttgtgaagaaatgccgtgagaaaagtaccggcctccagtatcccgccaaattc 129

Qy     130 atcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggagatcgagcgg 189
           ||||||||  ||  ||    | | |||||||| |||||||||| ||||| |||||||||
Db     130 atcaagaaaaggaggactaagtccagccggcggggtgtgagccgcgaggacatcgagcgg 189

Qy     190 gaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcacgacgtctat 249
           ||||| |||||||||  | || | | ||||| |||||||||||| |||||||| ||||||
Db     190 gaggtcagcatcctgaaggagatccagcaccccaatgtcatcaccctgcacgaggtctat 249

Qy     250 gagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagagctcttcgat 309
           ||||||   || |||||  | |  ||| | || || ||  | || || ||||| || ||
Db     250 gagaacaagacggacgtcatcctgatcttggaactcgttgcaggtggcgagctgtttgac 309

Qy     310 ttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcattaagcagatc 369
           ||| | ||  | ||||| ||  | | ||| ||||| || ||    ||  | || || ||
Db     310 ttcttagctgaaaaggaatctttaactgaagaggaagcaactgaatttctcaaacaaatt 369

Qy     370 ctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctcaagccagaa 429
           ||  |||| ||  ||||||| ||| |     |||| || |||||||||||| |||||  ||
Db     370 cttaatggtgtttactacctgcactcccttcaaatcgcccactttgatcttaagcctgag 429

Qy     430 aacattatgttgttagacaagaatattcccattccacacatcaagctgattgactttggt 489
           ||||| ||| | || || |  ||| | ||||  || |  |||||| | |||||||||
Db     430 aacataatgcttttggatagaaatgtccccaaacctcggatcaagatcattgactt---- 485

Qy     490 ctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacgccggaattt 549
                           ||||  ||||||||| || || |||||||| || || |||
Db     486 --------------------tggaaatgaatttaaaaacatatttgggactccagagttt 525

Qy     550 gttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatgtggagcata 609
           || ||||| || || || ||||| || || || ||||| ||||| || |||||||| ||
Db     526 gtcgctcctgagatagtcaactatgaacctcttggtcttgaggcagatatgtggagtatc 585

Qy     610 ggcgtcatcacctacatcctcttaagtggagcatccccttccctgggagacacgaagcag 669
           || || || ||||| |||||| ||||||| || ||||| || || |||||||| |||||
Db     586 ggggtaataacctatatcctcctaagtggggcctccccatttcttggagacactaagcaa 645

Qy     670 gaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattcttcagccat 729
           |||||  | |||||| |  |  | || |  ||||| ||||| || |||| ||||||  ||
Db     646 gaaacgttagcaaatgtatccgctgtcaactacgaatttgaggatgaatacttcagtaat 705

Qy     730 acgagcgagctggccaaggactttattcggaagcttctggttaaagagacccggaaacgg 789
           || || |  || ||||| || || ||  | |  |||||||| || ||  |   |||  |
Db     706 accagtgccctagccaaagatttcataagaagacttctggtcaaggatccaaagaagaga 765

Qy     790 ctcacaatccaagaggctctcagacacccctggatcacgccggtggacaaccagcaagcc 849
           | ||||| |||||   | |    || ||||||||||| |||    || |  || || ||
Db     766 atgacaattcaagatagtttgcagcatccctggatcaagcctaaagatacacaacaggca 825

Qy     850 atggtgcgacgggagtctgtggtcaatctggagaacttcaggaagcagtatgtccgcagg 909
           |     ||   |  || |  || ||  ||||||| |||| ||||      | ||| |
Db     826 cttagtagaaaagcatcagcagtaaacatggagaaattcaagaagtttgcagcccggaaa 885

Qy     910 cggtggaagctttccttcagcatcgtgtccctgtgcaaccacctcacccgctcgctgatg 969
           |||||  |  ||| |  || |  | || ||||||  |     |  || | ||  |  ||
Db     886 aaatggaaacaatccgttcgcttgatatcactgtgccaaagattatccaggtcattcctg 945

Qy     970 aagaaggtgcacctgag 986
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RESULT   9
AAQ89838
ID   AAQ89838 standard; cDNA; 5886 BP.
XX
AC   AAQ89838;
XX
DT   04-JAN-1980  (first entry)
XX
DE   Human death associated protein DAP-2.
XX
KW   Death associated protein; DAP; cytokine; cell death; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             337..4605
FT                   /*tag= a
FT                   /note= "claimed"
FT   polyA_signal    5628..5633
FT                   /*tag= b
FT   polyA_signal    5855..5860
FT                   /*tag= c
FT   misc_feature    5114..5118
FT                   /*tag= d
FT                   /label= instability motif
FT   misc_feature    5103..5107
FT                   /*tag= e
FT                   /label= instability motif
XX
PN   WO9510630-A.
XX
PD   20-APR-1995.
XX
PF   12-OCT-1994;   94WO-US11598.
XX
PR   12-OCT-1993;   93IL-0107250.
XX
PA   (RYCU/) RYCUS A.
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Kimchi A;
XX
DR   WPI; 1995-178528/23.
DR   P-PSDB; AAR74205.
XX
PT   DNA whose expression mediates cytokine-induced programmed cell
PT   death - used to treat diseases or disorders associated with
PT   uncontrolled, pathological cell growth or cytokine-induced
PT   programmed cell death.
XX
PS   Claim 2; Fig 8; 61pp; English.
XX
CC   DAP genes seem to play an imp. role in programmed cell death and the
CC   inhibition of their expression protects the cell from cytokine-
CC   promoted cell death. A cDNA library was generated from a mixture of
```

```
CC   mRNAs harvested after treatment of HeLa cells with IFN-gamma. It
CC   was cloned in antisense orientation into the EBV-based pTK01
CC   expression vector. The resulting expression library was introduced
CC   into HeLa cells. A fraction of the transfectants was selected with
CC   hygromycin B. The majority of transfected cells were selected with
CC   both hygromycin B and IFN-gamma. The cells that survived and/or
CC   grew in the presence of IFN-gamma were expanded and pooled. The
CC   extrachromosomal DNA was obtd. and cleaved with DpnI and introduced
CC   into E. coli HB101 host cells. A few bacterial clones were obtd.
CC   which included DNA antisense sequences, some of which were able to
CC   protect cells from the death-promoting effects of IFN-gamma.
CC   Plasmid DNAs were prepd. from 10 individual bacterial clones. PCR
CC   amplified cDNA inserts were generated from each plasmid using
CC   primers that corresp. to the immediate flanking sequence of the
CC   cDNA insertion sites in the pTK01 vector. The PCR fragments were
CC   used as labeled probes to seach Southern blots for possible cross
CC   hybridisation between some of the rescued antisense cDNA clones.
CC   The 10 cDNA clones were classified into six distinct
CC   non-overlapping gps., some constituting several members (clones)
CC   and some constituting a single member. Antisense cDNA clone 256 has
CC   the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and
CC   used to screen a K562 lambda gt10 cDNA library. The resulting
CC   composite sequence derived from 2 clones and the deduced AA sequence
CC   are shown in AAQ89838 and AAR74205. The ORF is also shown in AAQ89839.
CC   AAQ89838 has a poly A tail. The calculated mol. wt. of the protein
CC   is about 160 kDa. Several known domains and motifs were identified
CC   in the protein (see AAQ74205 FT).
XX
SQ   Sequence 5886 BP; 1447 A; 1524 C; 1500 G; 1415 T; 0 other;

  Query Match            41.5%;  Score 448.6;  DB 16;  Length 5886;
  Best Local Similarity  67.5%;  Pred. No. 7.7e-114;
  Matches  659;  Conservative    0;  Mismatches  294;  Indels   24;  Gaps    1;

Qy     10 ttcaagcagcagaaggtggaggacttttatgacatcggagaggagctggggagtggccag 69
          |||| |||| | || ||||| || |  || |||| ||| ||||| || || ||||| |||
Db    346 ttcaggcaggaaaacgtggatgattactacgacaccggcgaggaacttggcagtggacag 405

Qy     70 tttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgcagccaagttc 129
          |||||  | |||||||| ||||| ||||| || || || ||  ||||| | ||||| |||
Db    406 tttgcggttgtgaagaaatgccgtgagaaaagtaccggcctccagtatcccgccaaattc 465

Qy    130 atcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggagatcgagcgg 189
          ||||||||  ||  ||    | | |||||||| |||||||||| ||||| |||||||||
Db    466 atcaagaaaaggaggactaagtccagccggcggggtgtgagccgcgaggacatcgagcgg 525

Qy    190 gaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcacgacgtctat 249
          ||||| |||||||||  | || | | ||||| |||||||||||| |||||||| ||||||
Db    526 gaggtcagcatcctgaaggagatccagcaccccaatgtcatcaccctgcacgaggtctat 585

Qy    250 gagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagagctcttcgat 309
          ||||||   || |||||  | |  ||| | || || ||  | || || ||||| || ||
Db    586 gagaacaagacggacgtcatcctgatcttggaactcgttgcaggtggcgagctgtttgac 645

Qy    310 ttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcattaagcagatc 369
          ||| | ||  | ||||| ||  | | ||| ||||| || ||    ||  | || || ||
Db    646 ttcttagctgaaaaggaatctttaactgaagaggaagcaactgaatttctcaaacaaatt 705

Qy    370 ctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctcaagccagaa 429
          ||  |||| ||  ||||||| ||| |     |||| || |||||||||| ||||| ||
Db    706 cttaatggtgtttactacctgcactcccttcaaatcgcccactttgatcttaagcctgag 765

Qy    430 aacattatgttgttagacaagaatattcccattccacacatcaagctgattgactttggt 489
          ||||| ||| | || || |  ||| | |||  || |  |||||| | ||||||||
Db    766 aacataatgcttttggatagaaatgtccccaaacctcggatcaagatcattgactt---- 821

Qy    490 ctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacgccggaattt 549
                          ||||  |||||||||| || || |||||||| || || |||
Db    822 ----------------------tggaaatgaatttaaaaacatatttgggactccagagttt 861

Qy    550 gttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatgtggagcata 609
          || ||||| || || || ||||| || || || ||||| ||||| || |||||||| ||
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Db    862 gtcgctcctgagatagtcaactatgaacctcttggtcttgaggcagatatgtggagtatc 921

Qy    610 ggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagacacgaagcag 669
          || || || ||||| |||||| ||||||| || ||||| || || |||||||| |||||
Db    922 ggggtaataacctatatcctcctaagtggggcctccccatttcttggagacactaagcaa 981

Qy    670 gaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattcttcagccat 729
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Db    982 gaaacgttagcaaatgtatccgctgtcaactacgaatttgaggatgaatacttcagtaat 1041

Qy    730 acgagcgagctggccaaggactttattcggaagcttctggttaaagagacccggaaacgg 789
          || || |  || ||||| || || ||  | |  |||||||| || ||  |   |||  |
Db   1042 accagtgccctagccaaagatttcataagaagacttctggtcaaggatccaaagaagaga 1101

Qy    790 ctcacaatccaagaggctctcagacacccctggatcacgccggtggacaaccagcaagcc 849
          | ||||| |||||   | |    || ||||||||||| |||    || |  || || ||
Db   1102 atgacaattcaagatagtttgcagcatccctggatcaagcctaaagatacacaacaggca 1161

Qy    850 atggtgcgacgggagtctgtggtcaatctggagaacttcaggaagcagtatgtccgcagg 909
          |    ||   |  || |  || ||  ||||||| |||| ||||      | ||| |
Db   1162 cttagtagaaaagcatcagcagtaaacatggagaaattcaagaagtttgcagcccggaaa 1221

Qy    910 cggtggaagctttccttcagcatcgtgtccctgtgcaaccacctcacccgctcgctgatg 969
          |||||  |  ||| |  || |  | || ||||||  |     |  || | ||  |  ||
Db   1222 aaatggaaacaatccgttcgcttgatatcactgtgccaaagattatccaggtcattcctg 1281

Qy    970 aagaaggtgcacctgag 986
            |      || ||||
Db   1282 tccagaagtaacatgag 1298


RESULT  10
AAV60289
ID   AAV60289 standard; DNA; 5886 BP.
XX
AC   AAV60289;
XX
DT   12-JAN-1999  (first entry)
XX
DE   DNA sequence encoding death associated protein-2 (DAP-1, DAP-kinase).
XX
KW   Death associated protein; DAP-2; cell death; tumour cell; DAP-kinase;
KW   metastatic activity; cancer; psoriasis; autoimmune disease;
KW   programmed cell death; degenerative neurological disease;
KW   Alzheimer's; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             337..4608
FT                   /*tag=  a
FT                   /product= DAP-2
XX
PN   WO9839429-A2.
XX
PD   11-SEP-1998.
XX
PF   03-MAR-1998;   98WO-IL00102.
XX
PR   03-MAR-1997;   97US-0810712.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Kimchi A;
XX
DR   WPI; 1998-520781/44.
DR   P-PSDB; AAW71367.
XX
PT   New isolated death associated protein nucleic acids - used for the
PT   diagnosis and treatment or disorders associated with programmed cell
PT   death, e.g. cancers, auto:immune disease or neurological disease
XX
PS   Claim 2; Fig 8; 157pp; English.
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XX
CC   The present sequence encodes a death associated protein-2 (DAP-2,
CC   DAP-kinase). The DAP genes and proteins are used for promoting death of
CC   normal or tumour cells, and for suppressing the metastatic activity of
CC   tumour cells. They can be used in the treatment of diseases or disorders
CC   associated with uncontrolled pathological growth, e.g. cancer,
CC   psoriasis, autoimmune diseases and others. Agents which antagonise,
CC   inhibit or nuetralize DAP products are used for protecting cells from
CC   programmed cell death. In this case they can be used for the treatment
CC   of degenerative neurological diseases, e.g. Alzheimer's, prevention of
CC   death of T cells in AIDS patients, prevention of rejection associated
CC   cell death in transplants, and protection of normal cells from
CC   the cytotoxic effects of anti-cancer therapies.
XX
SQ   Sequence 5886 BP; 1447 A; 1525 C; 1499 G; 1415 T; 0 other;

  Query Match             41.5%;  Score 448.6;  DB 19;  Length 5886;
  Best Local Similarity   67.5%;  Pred. No. 7.7e-114;
  Matches  659;  Conservative    0;  Mismatches  294;  Indels   24;  Gaps    1;

Qy      10 ttcaagcagcagaaggtggaggacttttatgacatcggagaggagctggggagtggccag 69
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Db     346 ttcaggcaggaaaacgtggatgattactacgacaccggcgaggaacttggcagtggacag 405

Qy      70 tttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgcagccaagttc 129
           |||||  | |||||||| ||||| ||||| || || ||  ||||| | ||||| |||
Db     406 tttgcggttgtgaagaaatgccgtgagaaaagtaccggcctccagtatcccgccaaattc 465

Qy     130 atcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggagatcgagcgg 189
           ||||||||  ||  ||    | | |||||||| |||||||||| ||||| |||||||||
Db     466 atcaagaaaaggaggactaagtccagccggcggggtgtgagccgcgaggacatcgagcgg 525

Qy     190 gaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcacgacgtctat 249
           ||||| |||||||||  | || | | ||||| |||||||||||| |||||||| ||||||
Db     526 gaggtcagcatcctgaaggagatccagcaccccaatgtcatcaccctgcacgaggtctat 585

Qy     250 gagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagagctcttcgat 309
           ||||||   || |||||  | |  ||| | || || ||  | || || ||||| || ||
Db     586 gagaacaagacggacgtcatcctgatcttggaactcgttgcaggtggcgagctgtttgac 645

Qy     310 ttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcattaagcagatc 369
           ||| | ||  | ||||| ||  | | ||| ||||| || ||    ||  | || || ||
Db     646 ttcttagctgaaaaggaatctttaactgaagaggaagcaactgaatttctcaaacaaatt 705

Qy     370 ctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctcaagccagaa 429
           ||  |||| ||  ||||||| ||| |     |||| || |||||||||| ||||| ||
Db     706 cttaatggtgtttactacctgcactcccttcaaatcgcccactttgatcttaagcctgag 765

Qy     430 aacattatgttgttagacaagaatattcccattccacacatcaagctgattgactttggt 489
           ||||| ||| | || || |  ||| | ||||  || |  |||||| | ||||||||
Db     766 aacataatgcttttggatagaaatgtccccaaacctcggatcaagatcattgactt---- 821

Qy     490 ctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacgccggaattt 549
                               ||||  |||||||| || || |||||||| || || |||
Db     822 --------------------tggaaatgaatttaaaaacatatttgggactccagagttt 861

Qy     550 gttgctccagaaattgtgaactacgagcccctgggtctggaggctgacatgtggagcata 609
           || ||||| || || || ||||| || || || ||||| ||||| || |||||||| ||
Db     862 gtcgctcctgagatagtcaactatgaacctcttggtcttgaggcagatatgtggagtatc 921

Qy     610 ggcgtcatcacctacatcctcttaagtggagcatccccctttcctgggagacacgaagcag 669
           || || || ||||| |||||| ||||||| || ||||| || || |||||||| |||||
Db     922 ggggtaataacctatatcctcctaagtggggcctccccatttcttggagacactaagcaa 981

Qy     670 gaaacactggcaaatatcacatcagtgagttacgactttgatgaggaattcttcagccat 729
           |||||  | |||||| |  |  | || |  ||||| ||||| || |||| ||||||  ||
Db     982 gaaacgttagcaaatgtatccgctgtcaactacgaatttgaggatgaatacttcagtaat 1041

Qy     730 acgagcgagctggccaaggactttattcggaagcttctggttaaagagacccggaaacgg 789
           || || |  || ||||| || || ||  | |  |||||||| || ||  |   |||  |
Db    1042 accagtgccctagccaaagatttcataagaagacttctggtcaaggatccaaagaagaga 1101

Qy     790 ctcacaatccaagaggctctcagacacccctggatcacgccggtggacaaccagcaagcc 849
           | ||||| ||||||   | |    || |||||||||| |||    || |  || || ||
Db    1102 atgacaattcaagatagtttgcagcatccctggatcaagcctaaagatacacaacaggca 1161

Qy     850 atggtgcgacgggagtctgtggtcaatctggagaacttcaggaagcagtatgtccgcagg 909
           |     ||   |  || ||  ||||||| |||| ||||      | ||| |
Db    1162 cttagtagaaaagcatcagcagtaaacatggagaaattcaagaagtttgcagcccggaaa 1221

Qy     910 cggtggaagctttccttcagcatcgtgtccctgtgcaaccacctcacccgctcgctgatg 969
           |||||  |  ||| |  || |  | || |||||| |      |  || | ||  |  ||
Db    1222 aaatggaaacaatccgttcgcttgatatcactgtgccaaagattatccaggtcattcctg 1281

Qy     970 aagaaggtgcacctgag 986
           |      || ||||
Db    1282 tccagaagtaacatgag 1298


RESULT  11
AAZ99731
ID   AAZ99731 standard; cDNA; 480 BP.
XX
AC   AAZ99731;
XX
DT   12-JUL-2000  (first entry)
XX
DE   cDNA encoding human cardiovascular system associated protein kinase-4.
XX
KW   Human; cardiovascular system associated protein kinase-4; CSAPK-4;
KW   signalling pathway; cell growth; cell differentiation; gene mapping;
KW   tissue typing; forensic identification; cardiovascular disease;
KW   congestive heart failure; transgenic animal; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..480
FT                   /*tag=  a
FT                   /product= " cardiovascular system associated protein
FT                             kinase-4"
XX
PN   WO200014212-A1.
XX
PD   16-MAR-2000.
XX
PF   09-SEP-1999;   99WO-US20631.
XX
PR   09-SEP-1998;   98US-0099657.
PR   29-SEP-1998;   98US-0163115.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton S;
XX
DR   WPI; 2000-271053/23.
DR   P-PSDB; AAY84323.
XX
PT   New nucleic acid encoding cardiovascular system associated protein
PT   kinase, used e.g. for diagnosis, treatment and prevention of
PT   cardiovascular disease -
XX
PS   Claim 1; Page 149; 163pp; English.
XX
CC   The present sequence encodes a human cardiovascular system associated
CC   protein kinase-4 (CSAPK-4). CSAPK polypeptides are involved in signalling
CC   pathways associated with cell growth and differentiation. The CSAPK
CC   polypeptides and polynucleotides are used to screen for agents that
CC   specifically modulate CSAPK, which are potential therapeutic agents.
CC   They are also used for diagnosis, prognosis or monitoring of
CC   CSAPK-related diseases, gene mapping, tissue typing and forensic
CC   identification, and for treating or preventing disorders associated
CC   with aberrant CSAPK expression or activity, especially cardiovascular
CC   diseases such as congestive heart failure. They can also be used in
CC   pharmacogenomics. The CSAPK polynucleotide may also be used to generate
```

```
CC   transgenic animals.
XX
SQ   Sequence 480 BP; 123 A; 128 C; 137 G; 92 T; 0 other;


  Query Match             41.2%;  Score 445.4;  DB 21;  Length 480;
  Best Local Similarity   98.7%;  Pred. No. 1.8e-113;
  Matches  449;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     626 tcctcttaagtggagcatccccctttcctgggagacacgaagcaggaaacactggcaaata 685
           ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 tcagcttaagtggagcatccccctttcctgggagacacgaagcaggaaacactggcaaata 85

Qy     686 tcacatcagtgagttacgactttgatgaggaattcttcagccatacgagcgagctggcca 745
           ||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db      86 tcacagcagtgagttacgactttgatgaggaattcttcagccagacgagcgagctggcca 145

Qy     746 aggactttattcggaagcttctggttaaagagacccggaaacggctcacaatccaagagg 805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     146 aggactttattcggaagcttctggttaaagagacccggaaacggctcacaatccaagagg 205

Qy     806 ctctcagacacccctggatcacgccggtggacaaccagcaagccatggtgcgacgggagt 865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db     206 ctctcagacacccctggatcacgccggtggacaaccagcaagccatggtgcgcagggagt 265

Qy     866 ctgtggtcaatctggagaacttcaggaagcagtatgtccgcaggcggtggaagctttcct 925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     266 ctgtggtcaatctggagaacttcaggaagcagtatgtccgcaggcggtggaagctttcct 325

Qy     926 tcagcatcgtgtccctgtgcaaccacctcacccgctcgctgatgaagaaggtgcacctga 985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326 tcagcatcgtgtccctgtgcaaccacctcacccgctcgctgatgaagaaggtgcacctga 385

Qy     986 ggccggatgaggacctgaggaactgtgagagtgacactgaggaggacatcgccaggagga 1045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     386 ggccggatgaggacctgaggaactgtgagagtgacactgaggaggacatcgccaggagga 445

Qy    1046 aagccctccacccacggaggaggagcagcacctcc 1080
           ||||||||||||||||||||||||||||||||||
Db     446 aagccctccacccacggaggaggagcagcacctcc 480


RESULT  12
AAZ99730
ID   AAZ99730 standard; cDNA; 1864 BP.
XX
AC   AAZ99730;
XX
DT   12-JUL-2000  (first entry)
XX
DE   cDNA encoding human cardiovascular system associated protein kinase-4.
XX
KW   Human; cardiovascular system associated protein kinase-4; CSAPK-4;
KW   signalling pathway; cell growth; cell differentiation; gene mapping;
KW   tissue typing; forensic identification; cardiovascular disease;
KW   congestive heart failure; transgenic animal; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             275..757
FT                   /*tag= a
FT                   /product= " cardiovascular system associated protein
FT                            kinase-4"
XX
PN   WO200014212-A1.
XX
PD   16-MAR-2000.
XX
PF   09-SEP-1999;   99WO-US20631.
XX
PR   09-SEP-1998;   98US-0099657.
PR   29-SEP-1998;   98US-0163115.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Acton S;
XX
DR   WPI; 2000-271053/23.
DR   P-PSDB; AAY84323.
XX
PT   New nucleic acid encoding cardiovascular system associated protein
PT   kinase, used e.g. for diagnosis, treatment and prevention of
PT   cardiovascular disease -
XX
PS   Claim 1; Fig 4; 163pp; English.
XX
CC   The present sequence encodes a human cardiovascular system associated
CC   protein kinase-4 (CSAPK-4). CSAPK polypeptides are involved in signalling
CC   pathways associated with cell growth and differentiation. The CSAPK
CC   polypeptides and polynucleotides are used to screen for agents that
CC   specifically modulate CSAPK, which are potential therapeutic agents.
CC   They are also used for diagnosis, prognosis or monitoring of
CC   CSAPK-related diseases, gene mapping, tissue typing and forensic
CC   identification, and for treating or preventing disorders associated
CC   with aberrant CSAPK expression or activity, especially cardiovascular
CC   diseases such as congestive heart failure. They can also be used in
CC   pharmacogenomics. The CSAPK polynucleotide may also be used to generate
CC   transgenic animals.
XX
SQ   Sequence 1864 BP; 437 A; 504 C; 527 G; 396 T; 0 other;


  Query Match             41.2%;  Score 445.4;  DB 21;  Length 1864;
  Best Local Similarity   98.7%;  Pred. No. 3.4e-113;
  Matches  449;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     626 tcctcttaagtggagcatccccctttcctgggagacacgaagcaggaaacactggcaaata 685
           ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     300 tcagcttaagtggagcatccccctttcctgggagacacgaagcaggaaacactggcaaata 359

Qy     686 tcacatcagtgagttacgactttgatgaggaattcttcagccatacgagcgagctggcca 745
           ||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     360 tcacagcagtgagttacgactttgatgaggaattcttcagccagacgagcgagctggcca 419

Qy     746 aggactttattcggaagcttctggttaaagagacccggaaacggctcacaatccaagagg 805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     420 aggactttattcggaagcttctggttaaagagacccggaaacggctcacaatccaagagg 479

Qy     806 ctctcagacacccctggatcacgccggtggacaaccagcaagccatggtgcgacgggagt 865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db     480 ctctcagacacccctggatcacgccggtggacaaccagcaagccatggtgcgcagggagt 539

Qy     866 ctgtggtcaatctggagaacttcaggaagcagtatgtccgcaggcggtggaagctttcct 925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 ctgtggtcaatctggagaacttcaggaagcagtatgtccgcaggcggtggaagctttcct 599

Qy     926 tcagcatcgtgtccctgtgcaaccacctcacccgctcgctgatgaagaaggtgcacctga 985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 tcagcatcgtgtccctgtgcaaccacctcacccgctcgctgatgaagaaggtgcacctga 659

Qy     986 ggccggatgaggacctgaggaactgtgagagtgacactgaggaggacatcgccaggagga 1045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 ggccggatgaggacctgaggaactgtgagagtgacactgaggaggacatcgccaggagga 719

Qy    1046 aagccctccacccacggaggaggagcagcacctcc 1080
           ||||||||||||||||||||||||||||||||||
Db     720 aagccctccacccacggaggaggagcagcacctcc 754


RESULT  13
AAK91856
ID   AAK91856 standard; cDNA; 757 BP.
XX
AC   AAK91856;
XX
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DT 06-NOV-2001 (first entry)
XX
DE Human cDNA 5'-end sequence, SEQ ID NO: 316.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 2; SEQ ID NO 316; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is the nucleotide
CC sequence of the 5'-end of a cDNA provided in the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 757 BP; 176 A; 219 C; 220 G; 133 T; 9 other;

Query Match 35.6%; Score 385; DB 22; Length 757;
Best Local Similarity 75.6%; Pred. No. 1.3e-96;
Matches 511; Conservative 0; Mismatches 162; Indels 3; Gaps 3;

```
Qy      1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
          |||    | ||||  ||||  ||  | |||||||||  ||||||  ||  ||  ||||||||||
Db     70 atgtccacgttcaggcaggaggacgtggaggaccattatgagatgggggaggagctgggc 129

Qy     61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
          ||  ||||||||||| ||||||  ||||||||||| |||||  |||||||    |||||  |||
Db    130 agcggccagtttgcgatcgtgcggaagtgccggcagaagggcacgggcaaggagtacgca 189

Qy    121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
          ||||||||||||||||||||  |         | ||||||||  ||  ||||||||||||||||
Db    190 gccaagttcatcaagaagcgccgcctgtcatccagccggcgtggggtgagccgggaggag 249

Qy    181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
          ||||||||||||||||  ||||||||||  ||  |  |  |||||  |||  |||||||  ||||||
Db    250 atcgagcgggaggtgaacatcctgcgggagatccggcaccccaacatcatcaccctgcac 309

Qy    241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
          |||  |||  ||||||   ||  ||||||||  |  ||||||  |||||  ||  |||||  ||  |||
Db    310 gacatcttcgagaacaagacggacgtggtcctcatcctggagctggtctctggcggggag 369

Qy    301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
          |||||  ||  ||||||||  ||||||||||  ||||  |||||  ||  ||||||   |||  |
Db    370 ctctttgacttcctggcggagaaggagtcgctgacggaggacgaagccacccagttcctc 429

Qy    361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
          ||||||||||||||  ||  ||  |||||||  |||  |  |||   ||  ||  ||||||||  ||
Db    430 aagcagatcctggacggcgttcactacctgcactctaagcgcatcgcacactttgacctg 489

Qy    421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
          |||||  ||||||||  |||  ||  |  ||||||||   |  ||||  ||||  ||||||||  ||
Db    490 aagccggaaaacatcatgctgctggacaagaacgtgcccaacccacgaatcaagctcatc 549

Qy    481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
          |||||  ||   |  ||  |||  |  ||  ||  |   ||    |||||  ||  ||  ||  ||  ||
Db    550 gacttcggcatcgcncacaagatcgangcggggaacgaattcaanaacatcttcggcacc 609

Qy    541 ccggaa-tttgttgctccagaaattgtgaactacgagcccctgggtc-tggaggctgaca 598
          ||||||  |||||  ||  |||  ||||||||||||||  ||  ||  |||||  |  ||||  ||  ||||
Db    610 ccggaattttgtggccccanaaattgtgaactatgaaccgctgggccttggaagcngaca 669

Qy    599 tgtggagcataggcgtcatcacctacatcctcttaagtggagcat-ccccttttcctggga 657
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Db    670 tgttgaacatccgtgtctcccctatatcctcctgaaccggtgcatcccccttttcctgggc 729

Qy    658 gacacgaagcaggaaa 673
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Db    730 aaaaccaacnaggana 745
```

RESULT 14
AAK93262
ID AAK93262 standard; cDNA; 757 BP.
XX
AC AAK93262;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human cDNA clone representative sequence, SEQ ID NO: 1722.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Example 11; SEQ ID NO 1722; 1380pp + sequence listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence was used as the
CC representative sequence from a human clone which was used in
CC homology searches to identify the clone.

```
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ   Sequence 757 BP; 176 A; 219 C; 220 G; 133 T; 9 other;


  Query Match           35.6%;  Score 385;  DB 22;  Length 757;
  Best Local Similarity  75.6%;  Pred. No. 1.3e-96;
  Matches  511;  Conservative    0;  Mismatches  162;  Indels    3;  Gaps    3;

Qy       1 atggagccattcaagcagcagaaggtggaggacttttatgacatcggagaggagctgggg 60
           |||    | |||| |||| || | |||||||||  |||||| || || ||||||||||
Db      70 atgtccacgttcaggcaggaggacgtggaggaccattatgagatgggggaggagctgggc 129

Qy      61 agtggccagtttgccatcgtgaagaagtgccgggagaagagcacggggcttgagtatgca 120
           || |||||||||| ||||||  |||||||||| ||||| |||||||    ||||| |||
Db     130 agcggccagtttgcgatcgtgcggaagtgccggcagaagggcacgggcaaggagtacgca 189

Qy     121 gccaagttcatcaagaagcggcagagccgggcgagccggcgcggtgtgagccgggaggag 180
           |||||||||||||||||| |         | |||||||| || ||||||||||||||||
Db     190 gccaagttcatcaagaagcgccgcctgtcatccagccggcgtggggtgagccgggaggag 249

Qy     181 atcgagcgggaggtgagcatcctgcggcaggtgctgcaccacaatgtcatcacgctgcac 240
           |||||||||||||||| |||||||||| || | | ||||| |||  ||||||| ||||||
Db     250 atcgagcgggaggtgaacatcctgcgggagatccggcaccccaacatcatcaccctgcac 309

Qy     241 gacgtctatgagaaccgcaccgacgtggtgcacatccttgagctagtgtctggaggagag 300
           ||| |||  ||||||   || |||||||| | |||||| ||||| || ||||| || |||
Db     310 gacatcttcgagaacaagacggacgtggtcctcatcctggagctggtctctggcggggag 369

Qy     301 ctcttcgatttcctggcccagaaggagtcactgagtgaggaggaggccaccagcttcatt 360
           ||||| || |||||||| ||||||||| |||| ||||| || ||||||   ||| |
Db     370 ctctttgacttcctggcggagaaggagtcgctgacggaggacgaagccacccagttcctc 429

Qy     361 aagcagatcctggatggggtgaactaccttcacacaaagaaaattgctcactttgatctc 420
           |||||||||||||| || ||  ||||||| ||| | |||   || || |||||||| ||
Db     430 aagcagatcctggacggcgttcactacctgcactctaagcgcatcgcacactttgacctg 489

Qy     421 aagccagaaaacattatgttgttagacaagaatattcccattccacacatcaagctgatt 480
           ||||| |||||||| ||| || | |||||||| | |||| |||| ||||||||| ||
Db     490 aagccggaaaacatcatgctgctggacaagaacgtgcccaacccacgaatcaagctcatc 549

Qy     481 gactttggtctggctcacgaaatagaagatggagttgaatttaagaatatttttgggacg 540
           ||||| ||  | || ||| | || || |  ||    ||||| || || || || || ||
Db     550 gacttcggcatcgcncacaagatcgangcggggaacgaattcaanaacatcttcggcacc 609

Qy     541 ccggaa-tttgttgctccagaaattgtgaactacgagcccctgggtc-tggaggctgaca 598
           |||||| ||||| || ||| |||||||||||||| || || ||||| | |||| || ||||
Db     610 ccggaattttgtggccccanaaattgtgaactatgaaccgctgggccttggaagcngaca 669

Qy     599 tgtggagcataggcgtcatcacctacatcctcttaagtggagcat-ccccttttcctggga 657
           ||| || |||  | |||  | |      |  || ||  || |||| ||||||||||||||
Db     670 tgttgaacatccgtgtctcccctatatcctcctgaaccggtgcatccccctttcctgggc 729

Qy     658 gacacgaagcaggaaa 673
             | || ||  |||| |
Db     730 aaaaccaacnaggana 745


RESULT  15
AAK70641
ID   AAK70641 standard; DNA; 12638 BP.
XX
AC   AAK70641;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25453.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200157182-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01354.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.
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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-483426/52.
XX
PT   Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating cancers and
PT   metastasis -
XX
PS   Disclosure; SEQ ID NO 25453; 3071pp + Sequence Listing; English.
XX
CC   AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC   amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC   activity, and can be used in gene therapy and vaccine production. (I)
CC   proteins and polynucleotides may be used in the prevention, diagnosis and
CC   treatment of diseases associated with inappropriate (I) expression. For
CC   example, they may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of (I) by expressing inactive proteins or to
CC   supplement the patients own production of (I). Additionally, (I)
CC   polynucleotides may be used to produce the secreted (I), by inserting
CC   the nucleic acids into a host cell and culturing the cell to express the
CC   protein. (I) proteins and polynucleotides may be used to prevent,
CC   diagnose and treat immune/haematopoietic-related diseases, especially
CC   cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC   to AAK87694 represent human immune/haematopoietic antigen genomic
CC   sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 12638 BP; 2397 A; 3383 C; 3994 G; 2864 T; 0 other;

  Query Match           22.6%;  Score 244.6;  DB 22;  Length 12638;
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